CLAIMS

1. Isolated nucleic acid fragment, encoding a protein capable of binding to the AT2 receptor, which fragment is selected from the group consisting of the sequences SEQ ID NO:1, 3, 5, 7 and 9.

2. Fragment of one of the sequences according to Claim 1, comprising between 20 and 400 bp, useful as probes or as primers, for the detection of the sequences SEQ ID NO:1, 3, 5, 7 or 9, or of homologous sequences.

3. Fragment according to Claim 2, characterized in that it comprises from 20 bp to 400 bp included in the sequences SEQ ID NO:1, 3, 5, 7 or 9.

4. Fragment according to Claim 2 or Claim 3, characterized in that it is selected from the group consisting of the sequences SEQ ID NO:5, SEQ ID NO:10, SEQ ID NO:11 and SEQ ID NO:12.

5. Transcripts, characterized in that they are complementary to the sequences according to Claim 1.

6. Purified and isolated protein, which is capable of interacting with the AT2 receptor and which is selected from the group consisting of the sequences SEQ ID NO:2, 4, 6 or 8, which protein is called ATIP.

7. Translational product, characterized in that it is encoded by a nucleotide sequence according to Claim 1.

8. Antibodies, characterized in that they are directed against a protein or a protein fragment according to Claim 6 or Claim 7.

9. Recombinant cloning and/or expression vector, characterized in that it comprises a nucleotide sequence according to Claim 1.

10. Transformed host cell, characterized in that it comprises a vector according to Claim 9.

11. Transformed host cells, characterized in that they consist of a suitable yeast strain cotransformed with at least two vectors which respectively encode (i)

a so-called bait protein selected from the group consisting of a fragment containing at least SEQ ID NO:5 of the ATIP protein according to Claim 6 or Claim 7, and a fragment containing at least the C-terminal end of the AT2 receptor, which bait protein is fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the same transcription factor and (ii) a so-called prey protein, selected from the group consisting of a fragment containing at least SEQ ID NO:5 of the ATIP protein according to Claim 6 or Claim 7, a fragment containing at least the C-terminal end of the AT2 receptor and any other polypeptide corresponding to a sequence contained in a cDNA library, which prey protein is fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the same transcription factor, which vectors comprise, in addition, selectable markers.

12. Transformed host cell according to Claim 11, characterized in that it consists of a suitable yeast strain cotransformed with three vectors which respectively encode (i) a bait corresponding to a fragment containing the C-terminal end of the AT2 receptor fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the said transcription factor, (ii) a fragment containing at least SEQ ID NO:5 of the ATIP protein according to Claim 6 or Claim 7, fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the said transcription factor and (iii) a polypeptide corresponding to a sequence contained in a cDNA library, which vectors comprise, in addition, selectable markers.

13. Transformed host cell according to Claim 11, characterized in that it consists of a suitable yeast

strain cotransformed with two vectors which respectively encode (i) a fragment containing at least the sequence SEQ ID NO:5 of the ATIP protein according to Claim 6 or Claim 7, fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the said transcription factor and (ii) a polypeptide corresponding to a sequence contained in a cDNA library, fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the said transcription factor, which vectors comprise, in addition, selectable markers.

14. Transformed host cell according to Claim 11, characterized in that it consists of a suitable yeast strain cotransformed with two vectors, namely (i) a vector encoding a fragment containing at least the SEQ ID NO:5 of the ATIP protein sequence according to Claim 6, mutated or not, fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the said transcription factor and (ii) a vector encoding a fragment containing the C-terminal end of the AT2 receptor, mutated or not, fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the said transcription factor, which vectors comprise, in addition, selectable markers, one of the two vectors necessarily encoding a mutated protein.

15. Method for selecting proteins inhibiting ATIP protein according to Claim 6 or Claim 7-AT2 receptor interaction, which method comprises:

(a) cotransforming a suitable yeast strain with three vectors which respectively encode (i) a bait corresponding to a fragment containing the C-terminal end of the AT2 receptor fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the

said transcription factor, (ii) a fragment containing at least SEQ ID NO:5 of the ATIP protein according to Claim 6 or Claim 7, fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the said transcription factor and (iii) a polypeptide corresponding to a sequence contained in a cDNA library, which vectors comprise, in addition, selectable markers,

(b) selecting the clones of cDNA library expressing a polypeptide inhibiting the AT2 receptor-ATIP protein according to Claim 6 or Claim 7 interaction, on an appropriate selective medium, and

(c) identifying the said polypeptide.

16. Method for screening polypeptides interacting with the ATIP protein according to Claim 6 or Claim 7, which method comprises:

(a) cotransforming a suitable yeast strain with two vectors as defined above, namely which respectively encode (i) a fragment containing at least SEQ ID NO:5 of the ATIP protein according to Claim 6 or Claim 7, fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the said transcription factor and (ii) a polypeptide corresponding to a sequence contained in a cDNA library, fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the said transcription factor, which vectors comprise, in addition, selectable markers, and

(b) selecting the clones expressing a polypeptide interacting with the ATIP protein according to Claim 6 or Claim 7, on a suitable selective medium.

17. Method for characterizing the domains involved in the ATIP protein-AT2 receptor interaction, characterized in that it comprises:

(a) cotransforming a suitable yeast strain with two vectors, namely (i) a vector encoding a fragment

containing at least SEQ ID NO:5 of the ATIP protein according to Claim 6, mutated or not, fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the said transcription factor and (ii) a vector encoding a fragment containing the C-terminal end of the AT2 receptor, mutated or not, fused with a protein selected from the group consisting of the DNA-binding domain of a transcription factor and the activation domain of the said transcription factor, which vectors comprise, in addition, selectable markers, one of the two vectors necessarily encoding a mutated protein, and

(b) visualizing, by selection on a suitable selective medium, the possible loss of the ATIP protein according to Claim 6 or Claim 7-AT2 receptor interaction.

18. Method for selecting substances capable of influencing the ATIP protein according to Claim 6 or Claim 7-AT2 receptor interaction, which method comprises:

(a) bringing the ATIP protein according to Claim 6 or Claim 7, attached to a support, into contact with a fusion protein AT2 receptor-protein tag, optionally in the presence of a substance to be tested,

(b) at least one washing of the said support thus treated with a suitable buffer, and

(c) visualizing the possible ATIP protein according to Claim 6 or Claim 7-AT2 receptor interaction, in particular in SDS-PAGE, followed by immunoblotting with antibodies directed against the protein tag, fused with the AT2 receptor.

19. Method for selecting substances capable of interacting with the ATIP protein according to Claim 6 or Claim 7, characterized in that it comprises:

(a) bringing the ATIP protein according to Claim 6 or Claim 7, attached to a support, into contact with a cell lysate,

(b) at least one washing of the said support thus treated with a suitable buffer,

(c) visualizing the possible protein combined with the ATIP protein, in particular in SDS-PAGE, followed by immunoblotting with appropriate antibodies, and

(d) identifying the protein in the cell lysate interacting with the ATIP protein.

20. Use of the cotransformed cells according to any one of Claims 10 to 13, for the selection and screening of substances or of proteins capable of influencing the ATIP protein-AT2 receptor interaction or capable of interacting with the ATIP protein.